

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2000, 02:31:50 ; Search time 78.25 Seconds  
(without alignments)  
2.997 Million cell updates/sec

Title: US-09-185-908-2

Sequence: 1 IYSY 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues  
1 number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pIR\_63:\*  
2: pIR1:\*  
3: pIR2:\*  
4: pIR3:\*  
5: pIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	47	2	D64402
2	22	100.0	89	2	I52695
3	22	100.0	91	2	S51643
4	22	100.0	91	2	S55734
5	22	100.0	92	2	T03677
6	22	100.0	95	2	S00966
7	22	100.0	97	2	PH1068
8	22	100.0	98	2	PH1069
9	22	100.0	99	2	S59145
10	22	100.0	101	2	S20810
11	22	100.0	101	2	G72308
12	22	100.0	106	2	B47329
13	22	100.0	106	2	E72750
14	22	100.0	107	2	S24290
15	22	100.0	108	1	KVMS49
16	22	100.0	108	1	KVRB2K
17	22	100.0	119	2	C69525
18	22	100.0	119	2	A53257
19	22	100.0	121	2	S17861
20	22	100.0	122	2	S62781
21	22	100.0	122	2	JX0063
22	22	100.0	122	2	A29290
23	22	100.0	125	2	S49604
24	22	100.0	128	2	S31488
25	22	100.0	134	2	S11245
26	22	100.0	134	2	B69156
27	22	100.0	137	2	S22388
28	22	100.0	138	2	S59522
29	22	100.0	138	2	S29298

30	22	100.0	141	2	S74804	hypothetical prote
31	22	100.0	145	2	S51907	cryptogene protein
32	22	100.0	146	1	PSDG	phospholipase A2 (
33	22	100.0	146	2	I47184	ig heavy chain var
34	22	100.0	148	2	S75756	hypothetical prote
35	22	100.0	149	2	C71087	hypothetical prote
36	22	100.0	150	1	W6WL6	E6 protein - human
37	22	100.0	150	2	F59105	hypothetical prote
38	22	100.0	153	2	A53361	thyroxine-binding
39	22	100.0	155	2	C34965	hypothetical 17k p
40	22	100.0	155	2	S15576	lppi protein - Shl
41	22	100.0	171	2	A70203	hypothetical prote
42	22	100.0	172	2	D75017	n-terminal acetyl
43	22	100.0	172	2	A71455	probable acetyl
44	22	100.0	182	2	I54222	housekeeping prote
45	22	100.0	183	2	A64009	hypothetical prote

## ALIGNMENTS

RESULT 1  
D64402  
hypothetical protein M00820 - Methanococcus jannaschii  
C:Species: Methanococcus jannaschii  
C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 22-Oct-1999  
C:Accession: D64402  
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak  
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weissbrock, K.G.; Merrick, J.M.; Glodek,  
; Ron, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
Science 273, 1058-1073, -1996  
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese  
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc  
A:Reference number: A64300, M00820, M00820, M00820, M00820, M00820, M00820, M00820, M00820, M00820  
A:Accession: D64402  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-47 <BDU>  
A:Cross-references: GB:U67526; GB:L77117; NID:g1591508; PIDN:AAB98832.1; PID:g1591509  
C:Genetics:  
A:Map position: REV742333-742190  
A:Start codon: GTG

Query Match 100.0%; Score 22; DB 2; Length 47;  
Best Local Similarity 100.0%; Pred. NO. 84;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IYSY 4  
Db 33 IYSY 36

RESULT 2  
I52695  
Cyclin-dependent kinase 4 (EC 2.7.1.1) - human (fragment)  
M:Alternate names: protein-serine kinase CDK4  
C:Species: Homo sapiens (man)  
C>Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 10-Jul-1998  
C:Accession: I52695  
R:Rathb, Z.A.; Matsushima, H.; Valentine, M.; Shapiro, D.N.; Sherr, C.J.; Look, A.T.  
Cancer Res. 53, 5535-5541, 1993  
A:Title: Cloning and characterization of the CDK4 gene with MDM2 and GLI in human sarcomas.  
A:Reference number: I52695; M00820, M00820, M00820, M00820, M00820, M00820, M00820, M00820, M00820, M00820  
A:Accession: I52695  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-89 <RES>  
A:Cross-references: GB:S67448; NID:g456768  
C:Genetics:  
A:Gene: GDB:CDK4  
A:Cross-references: GDB:204022; OMIM:123829  
A:Map position: 12q13-12q13

C:Introns: 24/3; 80/3  
C:Superfamily: kinase-related transforming protein; protein kinase homology  
C:Keywords: Phosphotransferase  
C:1-89/Domain: protein kinase homology (fragment) <KIN>  
Query Match  
Best Local Similarity 100.0%; Score 22; DB 2; Length 89;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 IYSY 4  
|||  
70 IYSY 73  
RESULT 3  
S51643  
-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - garden pea (fragment)  
C:Species: Pisum sativum (garden pea)  
C:Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 03-Dec-1999  
C:Accession: S51643  
C:Submitted to the EMBL Data Library, December 1994  
C:Description: Sequential induction of ethylene biosynthetic enzymes by indole-3-acetic  
C:Reference number: S51643  
C:Status: preliminary  
C:Molecule type: mRNA  
C:Residues: 1-91 <PEC>  
C:Cross-references: EMBL:X83105; NID:9602079; PIDN:CAA58167.1; PID:9602080  
C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase  
C:Keywords: carbon-sulfur lyase; ethylene biosynthesis; S-adenosylmethionine  
Query Match  
Best Local Similarity 100.0%; Score 22; DB 2; Length 91;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 IYSY 4  
|||  
78 IYSY 81  
RESULT 4  
S5734  
-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) (clone ACS-2) - garden pea (fr  
C:Species: Pisum sativum (garden pea)  
C:Date: 28-Oct-1995 #sequence\_revision 24-May-1996 #text\_change 03-Dec-1999  
C:Accession: S5734  
C:Submitted to the EMBL Data Library, December 1995  
C:Description: Sequential induction of the ethylene biosynthetic enzymes by indole-3-acetic ac  
C:Reference number: S5734; MUID:95322591  
C:Status: not compared with conceptual translation  
C:Molecule type: mRNA  
C:Residues: 1-91 <PEC>  
C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase  
C:Keywords: carbon-sulfur lyase; ethylene biosynthesis; S-adenosylmethionine  
Query Match  
Best Local Similarity 100.0%; Score 22; DB 2; Length 91;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 IYSY 4  
|||  
78 IYSY 81  
RESULT 5  
03677  
-it2 protein (clone PAL141), PI starvation induced - common tobacco

C:Species: Nicotiana tabacum (common tobacco)  
C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 24-Mar-1999  
C:Accession: T03677  
C:Physiol. Plantarum 93, 11-18, 1995  
A:Title: Cloning and sequencing of the cDNAs induced by aluminium treatment and PI st  
A:Reference number: Z14998  
A:Accession: T03677  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-92 <EZA>  
A:Cross-references: EMBL:D29681; NID:d1019588; PID:d1006713  
A:Experimental source: strain Samsun; clone PAL141  
C:Genetics:  
A:Gene: pit2  
Query Match  
Best Local Similarity 100.0%; Score 22; DB 2; Length 92;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 IYSY 4  
|||  
48 IYSY 51  
RESULT 6  
S00966  
Hypothetical protein 8 - Yeast (Kluveromyces marxianus var. lactis) plasmid pgk12  
C:Species: Kluveromyces marxianus var. lactis, Candida sphaerica  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 29-Oct-1999  
C:Accession: S00966  
R:Tommasino, M.; Ricci, S.; Galeotti, C.L.  
Nucleic Acids Res. 16, 5863-5878, 1988  
A:Title: Genome organization of the killer plasmid pgk12 from Kluveromyces lactis.  
A:Reference number: S00959; MUID:88289339  
A:Accession: S00966  
A:Molecule type: DNA  
A:Residues: 1-95 <TOM>  
A:Cross-references: EMBL:X07776; NID:92868; PIDN:CAA30610.1; PID:92877  
C:Genetics:  
A:Genome: plasmid  
Query Match  
Best Local Similarity 100.0%; Score 22; DB 2; Length 95;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 IYSY 4  
|||  
37 IYSY 40  
RESULT 7  
PH1068  
Ig light chain V region (clone s17.166) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 15-Jun-1996  
C:Accession: PH1068  
R:Tillman, D.M.; Jou, N.T.; Hall, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective  
A:Reference number: PH0971; MUID:92381444  
A:Accession: PH1068  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-97 <TIL>  
A:Experimental source: B cell, strain [NZB x NZW]F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: Immunoglobulin  
Query Match  
Best Local Similarity 100.0%; Score 22; DB 2; Length 97;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 IYSY 4  
|||||  
Db 28 IYSY 31

## RESULT 8

PH1069  
Ig light chain V region (clone 185-cl) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 15-Jun-1996  
C:Accession: PH1069  
R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.  
J. Exp. Med. 176, 761-779, 1992  
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B  
A:Reference number: PH0971; MUID:92381444  
A:Accession: PH1069  
A:Status: nucleic acid sequence not shown  
A:Residues: 1-98 <TIL>  
A:Molecule type: mRNA  
A:Experimental source: B cell, strain (NZB x NZW)F1  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: Immunoglobulin

Query Match 100.0%; Score 22; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 IYSY 4  
|||||  
Db 29 IYSY 32

## RESULT 9

SS59145  
NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L - land snail mitochondrion  
C:Species: mitochondrion Albinaria coerulea (land snail)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 07-Dec-1999  
C:Accession: SS59145  
R:Hatzioglou, E.; Rodakis, G.C.; Lecanidou, R.  
Genetics 140, 1353-1366, 1995  
A:Title: Complete sequence and gene organization of the mitochondrial genome of the land  
A:Reference number: S59143; MUID:96120351  
A:Accession: S59145  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-99 <HAT>  
A:Cross-references: EMBL:X83390; NID:g975668; PIDN:CA58298.1; PID:g975671  
C:Genetics:  
A:Gene: ND4L  
A:Genome: mitochondrion  
A:Genetic code: SGC4  
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4L  
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 100.0%; Score 22; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSY 4  
|||||  
Db 3 IYSY 6

## RESULT 10

SS20810  
Ig kappa chain V region (hybridoma C8) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999

C:Accession: S20810  
R:Hoogenboom, H.; Dubois, P.; Raus, J.; Voelckaert, G.  
Submitted to the EMBL Data Library, September 1990  
A:Description: Nucleotide sequences of the variable region cDNAs encoding a murine an  
A:Reference number: S20809  
A:Accession: S20810  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-101 <HOO>

A:Cross-references: EMBL:X54693; NID:g50251; PIDN:CA538509.1; PID:g50252  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotetramer; Immunoglobulin

Query Match 100.0%; Score 22; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSY 4  
|||||  
Db 22 IYSY 25

## RESULT 11

G72308  
hypothetical protein - Thermotoga maritima (strain MSB8)  
C:Species: Thermotoga maritima  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999  
C:Accession: G72308  
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hic  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,  
C.M.  
Nature 399, 323-329, 1999  
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome  
A:Reference number: A72200; MUID:99287316  
A:Accession: G72308  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-101 <ARN>  
A:Cross-references: GB:AE001761; GB:AE000512; NID:g4981529; PID:g4981533; TIGR:TM0993  
A:Experimental source: strain MSB8  
C:Genetics:  
A:Gene: TM0993

Query Match 100.0%; Score 22; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSY 4  
|||||  
Db 77 IYSY 80

## RESULT 12

B47329  
Ig kappa chain V region (PRI) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 21-Sep-1993 #sequence\_revision 17-Jul-1994 #text\_change 16-Aug-1996  
C:Accession: B47329  
R:Brinkmann, U.; Gallo, M.; Brinkmann, E.; Kunwar, S.; Pastan, I.  
Proc. Natl. Acad. Sci. U.S.A. 90, 547-551, 1993  
A:Title: A recombinant immunotoxin that is active on prostate cancer cells and that i  
A:Reference number: A47329; MUID:93133825  
A:Accession: B47329  
A:Status: preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 1-106 <BR1>  
A:Experimental source: Balb/c  
A>Note: sequence modified after extraction from NCBI backbone  
A>Note: sequence extracted from NCBI backbone (NCBIN:122874)  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotetramer; Immunoglobulin

```
Query Match          100.0%; Score 22; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IYSY 4
|||||
29 IYSY 32

RESULT 13
Hypothetical protein APE0530 - Aeropyrum pernix (strain K1)
Species: Aeropyrum pernix
Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
Accession: E72750
Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahara, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kawai, Res. 6, 83-101, 1999
Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix strain K1
Reference number: A72450; MID:99310339
Accession: E72750
Status: preliminary
Molecule type: DNA
Residues: 1-106 <KAW>
Cross-references: DDBJ:AP000059; NID:95103911; PIDN:BA079497.1; PID:dl043283; PID:95103911
Experimental source: strain K1
Gene: APE0530

Query Match          100.0%; Score 22; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IYSY 4
|||||
63 IYSY 66

RESULT 14
Ig kappa chain V region (J534/32) - mouse
Accession: S24290
Species: Mus musculus (house mouse)
Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
Accession: S24290
Chenharmon, B.
Submitted to the EMBL Data Library, September 1991
Description: Cloning and sequencing of the cDNA coding for the variable regions of the kappa chain of mouse anti-lymphocyte antigen A2.4 monoclonal antibody.
Reference number: S24287
Accession: S24290
Status: preliminary
Molecule type: mRNA
Residues: 1-107 <MON>
Cross-references: EMBL:X62704; NID:951693; PIDN:CAA44580.1; PID:e42102; PID:g1333967
Superfamily: immunoglobulin V region; immunoglobulin homology
Keywords: heterotetramer; immunoglobulin

Query Match          100.0%; Score 22; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IYSY 4
|||||
29 IYSY 32

RESULT 15
Ig kappa chain V region (M149) - mouse
Accession: S24290
Species: Mus musculus (house mouse)
```

```
CDate: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 16-Aug-1996
CAccession: A01919
RAppella, E.; Alvarez, V.L.
Mol Immunol 17, 1507-1513, 1980
A:Title: Amino acid sequence of the variable region of M149 mouse myeloma light chain
A:Reference number: A01919; MID:82057806
A:Accession: A01919
A:Molecule type: protein
A:Residues: 1-108 <APP>
A:Experimental source: strain BALB/c
A>Note: this chain was isolated from a myeloma protein
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L) chains disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status predicted

Query Match          100.0%; Score 22; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IYSY 4
|||||
29 IYSY 32
```

Search completed: June 20, 2000, 02:31:52  
Job time: 8/785 sec